SEQUENCE LISTING

(1) GENERAL INFORMATION:

5   (i) APPLICANT: Genentech, Inc., Hsei, Vanessa
                       Koumenis, Iphigenia
                       Leong, Steven R.
                       Presta, Leonard G.
                       Shahrokh, Zahra
10   Zapata, Gerardo A.

     (ii) TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES
            AND HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES

15   (iii) NUMBER OF SEQUENCES: 72

     (iv) CORRESPONDENCE ADDRESS:
         (A) ADDRESSEE: Genentech, Inc.
         (B) STREET: 1 DNA Way
20   (C) CITY: South San Francisco
         (D) STATE: California
         (E) COUNTRY: USA
         (F) ZIP: 94080

25   (v) COMPUTER READABLE FORM:
         (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
         (B) COMPUTER: IBM PC compatible
         (C) OPERATING SYSTEM: PC-DOS/MS-DOS
         (D) SOFTWARE: WinPatin (Genentech)
30
     (vi) CURRENT APPLICATION DATA:
         (A) APPLICATION NUMBER:
         (B) FILING DATE: 20-Jan-1999
         (C) CLASSIFICATION:
35
   (vii) PRIOR APPLICATION DATA:
         (A) APPLICATION NUMBER: 60/074330
         (B) FILING DATE: 22-JAN-1998

40 (vii) PRIOR APPLICATION DATA:
         (A) APPLICATION NUMBER: 60/094003
         (B) FILING DATE: 24-JUL-1998

   (vii) PRIOR APPLICATION DATA:
45   (A) APPLICATION NUMBER: 60/094013
         (B) FILING DATE: 24-JUL-1998

   (vii) PRIOR APPLICATION DATA:
         (A) APPLICATION NUMBER: 60/075467
50   (B) FILING DATE: 20-FEB-1998

  (viii) ATTORNEY/AGENT INFORMATION:
         (A) NAME: Love, Richard B.
         (B) REGISTRATION NUMBER: 34,659
55   (C) REFERENCE/DOCKET NUMBER: P1085R4-1A

```
(ix) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE: 650/225-5530
     (B) TELEFAX: 650/952-9881
(2) INFORMATION FOR SEQ ID NO:1:
```

5

```
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 22 base pairs
         (B) TYPE: Nucleic Acid
         (C) STRANDEDNESS: Single
```

10

```
         (D) TOPOLOGY: Linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
```

15   CAGTCCAACT GTTCAGGACG CC 22

```
(2) INFORMATION FOR SEQ ID NO:2:
```

```
     (i) SEQUENCE CHARACTERISTICS:
```

20

```
         (A) LENGTH: 22 base pairs
         (B) TYPE: Nucleic Acid
         (C) STRANDEDNESS: Single
         (D) TOPOLOGY: Linear
```

25   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
     GTGCTGCTCA TGCTGTAGGT GC 22
```

30   (2) INFORMATION FOR SEQ ID NO:3:

```
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 23 base pairs
         (B) TYPE: Nucleic Acid
```

35   (C) STRANDEDNESS: Single

```
         (D) TOPOLOGY: Linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
```

40

```
     GAAGTTGATG TCTTGTGAGT GGC 23
```

```
(2) INFORMATION FOR SEQ ID NO:4:
```

45   (i) SEQUENCE CHARACTERISTICS:

```
         (A) LENGTH: 24 base pairs
         (B) TYPE: Nucleic Acid
         (C) STRANDEDNESS: Single
         (D) TOPOLOGY: Linear
```

50

```
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
```

```
     GCATCCTAGA GTCACCGAGG AGCC 24
```

55

```
(2) INFORMATION FOR SEQ ID NO:5:
```

244

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: Nucleic Acid
 5      (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10
    CACTGGCTCA GGGAAATAAC CC 22

(2) INFORMATION FOR SEQ ID NO:6:

15     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear
20
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:


    GGAGAGCTGG GAAGGTGTGC AC 22
25
(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35 base pairs
30      (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
35

    ACAAACGCGT ACGCTGACAT CGTCATGACC CAGTC 35

(2) INFORMATION FOR SEQ ID NO:8:
40
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
45      (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:


50  ACAAACGCGT ACGCTGATAT TGTCATGACT CAGTC 35

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
55      (A) LENGTH: 35 base pairs
        (B) TYPE: Nucleic Acid
```

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

5

ACAAACGCGT ACGCTGACAT CGTCATGACA CAGTC 35

(2) INFORMATION FOR SEQ ID NO:10:

10

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 37 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Single
15
       (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20
GCTCTTCGAA TGGTGGGAAG ATGGATACAG TTGGTGC 37

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
25
       (A) LENGTH: 39 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear

30   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGATGGGCCC GGATAGACCG ATGGGGCTGT TGTTTTGGC 39

35 (2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 39 base pairs
       (B) TYPE: Nucleic Acid
40
       (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

45
CGATGGGCCC GGATAGACTG ATGGGGCTGT CGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:13:

50   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 39 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear
55
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGATGGGCCC GGATAGACGG ATGGGGCTGT TGTTTTGGC 39

5   (2) INFORMATION FOR SEQ ID NO:14:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 39 base pairs
            (B) TYPE: Nucleic Acid
10   (C) STRANDEDNESS: Single
            (D) TOPOLOGY: Linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

15

CGATGGGCCC GGATAGACAG ATGGGGCTGT TGTTTTGGC 39

    (2) INFORMATION FOR SEQ ID NO:15:

20   (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 39 base pairs
            (B) TYPE: Nucleic Acid
            (C) STRANDEDNESS: Single
            (D) TOPOLOGY: Linear

25

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGATGGGCCC GGATAGACTG ATGGGGCTGT TGTTTTGGC 39

30

    (2) INFORMATION FOR SEQ ID NO:16:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 369 base pairs
35   (B) TYPE: Nucleic Acid
            (C) STRANDEDNESS: Double
            (D) TOPOLOGY: Linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

40

GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA 50

CAGGGTCAGC GTCACCTGCA AGGCCAGTCA GAATGTGGGT ACTAATGTAG 100

45

CCTGGTATCA ACAGAAACCA GGGCAATCTC CTAAAGCACT GATTTACTCG 150

TCATCCTACC GGTACAGTGG AGTCCCTGAT CGCTTCACAG GCAGTGGATC 200

50 TGGGACAGAT TTCACTCTCA CCATCAGCCA TGTGCAGTCT GAAGACTTGG 250

CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT 300

GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC 350

55

CATCTTCCCA CCATTCGAA 369

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 123 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val
 1               5                  10                  15

Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly
                20                  25                  30

Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
                35                  40                  45

Ala Leu Ile Tyr Ser Ser Ser Tyr Arg Tyr Ser Gly Val Pro Asp
                50                  55                  60

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                65                  70                  75

Ser His Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln
                80                  85                  90

Tyr Asn Ile Tyr Pro Leu Thr Phe Gly Pro Gly Thr Lys Leu Glu
                95                  100                 105

Leu Lys Arg Ala Asp Ala Ala Pro Pro Thr Val Ser Ile Phe Pro
                110                 115                 120

Pro Phe Glu
        123
```

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 417 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
TTCTATTGCT ACAAACGCGT ACGCTGAGGT GCAGCTGGTG GAGTCTGGGG 50

GAGGCTTAGT GCCGCCTGGA GGGTCCCTGA AACTCTCCTG TGCAGCCTCT 100

GGATTCATAT TCAGTAGTTA TGGCATGTCT TGGGTTCGCC AGACTCCAGG 150

CAAGAGCCTG GAGTTGGTCG CAACCATTAA TAATAATGGT GATAGCACCT 200
```

ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG AGACAATGCC 250

AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC 300

CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGGTT 350

ACTGGGGCCA AGGGACTCTG GTCACTGTCT CTGCAGCCAA AACAACAGCC 400

CCATCTGTCT ATCCGGG 417

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 130 amino acids
       (B) TYPE: Amino Acid
       (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Pro Pro Gly
 1               5                  10                  15

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser
                20                  25                  30

Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Ser Leu
                35                  40                  45

Glu Leu Val Ala Thr Ile Asn Asn Asn Gly Asp Ser Thr Tyr Tyr
                50                  55                  60

Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                65                  70                  75

Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp
                80                  85                  90

Thr Ala Met Phe Tyr Cys Ala Arg Ala Leu Ile Ser Ser Ala Thr
                95                  100                 105

Trp Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
                110                 115                 120

Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro
                125                 130
```

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 31 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

249

ACAAACGCGT ACGCTGATAT CGTCATGACA G 31

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 31 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGCATCAG CTCTTCGAAG CTCCAGCTTG G 31

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: DNA
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCACTAGTAC GCAAGTTCAC G 21

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATGGGCCCT TGGTGGAGGC TGCAGAGACA GTG 33

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 714 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50

TGCTACAAAC GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA 100

```
     TGTCCACATC AGTAGGAGAC AGGGTCAGCG TCACCTGCAA GGCCAGTCAG 150

 5   AATGTGGGTA CTAATGTAGC CTGGTATCAA CAGAAACCAG GGCAATCTCC 200

     TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGGA GTCCCTGATC 250

     GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT 300

10   GTGCAGTCTG AAGACTTGGC AGACTATTTC TGTCAGCAAT ATAACATCTA 350

     TCCTCTCACG TTCGGTCCTG GGACCAAGCT GGAGCTTCGA GAGCTGTGG 400

     CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT 450
15
     GGAACTGCTT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC 500

     CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG 550

20   AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC 600

     ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG 650

     CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA 700
25
     GGGGAGAGTG TTAA 714
```

(2) INFORMATION FOR SEQ ID NO:25:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 237 amino acids
     (B) TYPE: Amino Acid
     (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1           5                  10                  15

Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Val Met Thr Gln Ser
            20                  25                  30

Gln Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val Thr
                35                  40                  45

Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
                50                  55                  60

Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile Tyr Ser Ser Ser
                65                  70                  75

Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
                80                  85                  90

Gly Thr Asp Phe Thr Leu Thr Ile Ser His Val Gln Ser Glu Asp
                95                  100                 105
```

<div align="center">251</div>

```
     Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu Thr
                 110             115             120
```

5
```
     Phe Gly Pro Gly Thr Lys Leu Glu Leu Arg Arg Ala Val Ala Ala
                 125             130             135
```

```
     Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
                 140             145             150
```
10
```
     Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
                 155             160             165
```

```
     Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
                 170             175             180
```
15
```
     Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                 185             190             195
```

20
```
     Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
                 200             205             210
```

```
     Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
                 215             220             225
```
25
```
     Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                 230             235     237
```

(2) INFORMATION FOR SEQ ID NO:26:

30
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 756 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Double
35
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

40
```
ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50

TGCTACAAAC GCGTACGCTG AGGTGCAGCT GGTGGAGTCT GGGGGAGGCT 100

TAGTGCCGCC TGGAGGGTCC CTGAAACTCT CCTGTGCAGC CTCTGGATTC 150
```
45
```
ATATTCAGTA GTTATGGCAT GTCTTGGGTT CGCCAGACTC CAGGCAAGAG 200

CCTGGAGTTG GTCGCAACCA TTAATAATAA TGGTGATAGC ACCTATTATC 250
```
50
```
CAGACAGTGT GAAGGGCCGA TTCACCATCT CCCGAGACAA TGCCAAGAAC 300

ACCCTGTACC TGCAAATGAG CAGTCTGAAG TCTGAGGACA CAGCCATGTT 350

TTACTGTGCA AGAGCCCTCA TTAGTTCGGC TACTTGGTTT GGTTACTGGG 400
```
55
```
GCCAAGGGAC TCTGGTCACT GTCTCTGCAG CCTCCACCAA GGGCCCATCG 450
```

```
GTCTTCCCCC TGGCACCCTC CTCCAAGAGC ACCTCTGGGG GCACAGCGGC 500

CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCGT 550

GGAACTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA 600

CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG 650

CAGCTTGGGC ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA 700

ACACCAAGGT GGACAAGAAA GTTGAGCCCA AATCTTGTGA CAAAACTCAC 750

ACATGA 756
```

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 251 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1               5                  10                  15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
                 20                  25                  30

Gly Gly Gly Leu Val Pro Pro Gly Gly Ser Leu Lys Leu Ser Cys
                 35                  40                  45

Ala.Ala Ser Gly Phe Ile Phe Ser Ser Tyr Gly Met Ser Trp Val
                 50                  55                  60

Arg Gln Thr Pro Gly Lys Ser Leu Glu Leu Val Ala Thr Ile Asn
                 65                  70                  75

Asn Asn Gly Asp Ser Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg
                 80                  85              ·    90

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
                 95                  100                 105

Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Phe Tyr Cys Ala
                 110                 115                 120

Arg Ala Leu Ile Ser Ser Ala Thr Trp Phe Gly Tyr Trp Gly Gln
                 125                 130                 135

Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser
                 140                 145                 150

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
                 155                 160                 165
```

253

```
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
                170                 175             180

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                185                 190             195

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
                200                 205             210

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
                215                 220             225

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
                230                 235             240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
                245                 250 251
```

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCAATGCATA CGCTGACATC GTGATGACCC AGACCCC 37

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCAATGCATA CGCTGATATT GTGATGACTC AGACTCC 37

(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCAATGCATA CGCTGACATC GTGATGACAC AGACACC 37

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 35 base pairs
    (B) TYPE: Nucleic Acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGATGTCAAT TGCTCACTGG ATGGTGGGAA GATGG 35

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 32 base pairs
    (B) TYPE: Nucleic Acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAAACGCGTA CGCTGAGATC CAGCTGCAGC AG 32

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 32 base pairs
    (B) TYPE: Nucleic Acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAAACGCGTA CGCTGAGATT CAGCTCCAGC AG 32

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 391 base pairs
    (B) TYPE: Nucleic Acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATATCGTGA TGACACAGAC ACCACTCTCC CTGCCTGTCA GTCTTGGAGA 50

TCAGGCCTCC ATCTCTTGCA GATCTAGTCA GAGCCTTGTA CACGGTATTG 100

GAAACACCTA TTTACATTGG TACCTGCAGA AGCCAGGCCA GTCTCCAAAG 150

CTCCTGATCT ACAAAGTTTC CAACCGATTT TCTGGGGTCC CAGACAGGTT 200

5   CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAGGATC AGCAGAGTGG 250

AGGCTGAGGA TCTGGGACTT TATTTCTGCT CTCAAAGTAC ACATGTTCCG 300

CTCACGTTCG GTGCTGGGAC CAAGCTGGAG CTGAAACGGG CTGATGCTGC 350

10   ACCAACTGTA TCCATCTTCC CACCATCCAG TGAGCAATTG A 391

(2) INFORMATION FOR SEQ ID NO:35:

15   (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 131 amino acids
            (B) TYPE: Amino Acid
            (D) TOPOLOGY: Linear

20   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

         Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu
          1   5   10   15

25   Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val
                         20   25   30

         His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
                         35   40   45

30   Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
                         50   55   60

         Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                         65   70   75

35   Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu
                         80   85   90

         Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly Ala
                         95   100   105

40   Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro Thr Val
                         110   115   120

         Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Lys
                         125   130 131

         (2) INFORMATION FOR SEQ ID NO:36:
50
             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 405 base pairs
                 (B) TYPE: Nucleic Acid
                 (C) STRANDEDNESS: Single
55   (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGATTCAGC TGCAGCAGTC TGGACCTGAG CTGATGAAGC CTGGGGCTTC 50

AGTGAAGATA TCCTGCAAGG CTTCTGGTTA TTCATTCAGT AGCCACTACA 100

TGCACTGGGT GAAGCAGAGC CATGGAAAGA GCCTTGAGTG GATTGGCTAC 150

ATTGATCCTT CCAATGGTGA AACTACTTAC AACCAGAAAT TCAAGGGCAA 200

GGCCACATTG ACTGTAGACA CATCTTCCAG CACAGCCAAC GTGCATCTCA 250

GCAGCCTGAC ATCTGATGAC TCTGCAGTCT ATTTCTGTGC AAGAGGGGAC 300

TATAGATACA ACGGCGACTG GTTTTTCGAT GTCTGGGGCG CAGGGACCAC 350

GGTCACCGTC TCCTCCGCCA AAACCGACAG CCCCATCGGT CTATCCGGGC 400

CCATC 405

(2) INFORMATION FOR SEQ ID NO:37:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 135 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly
 1   5   10   15

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser
                20   25   30

Ser His Tyr Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu
                35   40   45

Glu Trp Ile Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr
                50   55   60

Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser
                65   70   75

Ser Ser Thr Ala Asn Val His Leu Ser Ser Leu Thr Ser Asp Asp
                80   85   90

Ser Ala Val Tyr Phe Cys Ala Arg Gly Asp Tyr Arg Tyr Asn Gly
                95   100   105

Asp Trp Phe Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val
                110   115   120

Ser Ser Ala Lys Thr Asp Ser Pro Ile Gly Leu Ser Gly Pro Ile
                125   130   135

257

(2) INFORMATION FOR SEQ ID NO:38:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTTGGTGGAG GCGGAGGAGA CG 22

(2) INFORMATION FOR SEQ ID NO:39:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 38 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAAACGGGCT GTTGCTGCAC CAACTGTATT CATCTTCC 38

(2) INFORMATION FOR SEQ ID NO:40:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 31 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 31

(2) INFORMATION FOR SEQ ID NO:41:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 729 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50

TGCTACAAAT GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC 100

TGCCTGTCAG TCTTGGAGAT CAGGCCTCCA TCTCTTGCAG ATCTAGTCAG 150

258

```
         AGCCTTGTAC ACGGTATTGG AAACACCTAT TTACATTGGT ACCTGCAGAA 200

         GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC AACCGATTTT 250
  5
         CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTCACA 300

         CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC 350

 10      TCAAAGTACA CATGTTCCGC TCACGTTCGG TGCTGGGACC AAGCTGGAGC 400

         TGAAACGGGC TGTTGCTGCA CCAACTGTAT TCATCTTCCC ACCATCCAGT 450

         GAGCAATTGA AATCTGGAAC TGCCTCTGTT GTGTGCCTGC TGAATAACTT 500
 15
         CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550

         CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600

 20      TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650

         CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700

         CAAAGAGCTT CAACAGGGGA GAGTGTTAA 729
 25
         (2) INFORMATION FOR SEQ ID NO:42:

             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 242 amino acids
                 (B) TYPE: Amino Acid
 30              (D) TOPOLOGY: Linear

             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

 35      Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
           1               5                  10                  15

         Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Val Met Thr Gln Thr
                           20                  25                  30
 40
         Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
                           35                  40                  45

         Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Asn Thr Tyr
 45                        50                  55                  60

         Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu
                           65                  70                  75

 50      Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
                           80                  85                  90

         Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg
                           95                  100                 105
 55
         Val Glu Ala Glu Asp Leu Gly Leu Tyr Phe Cys Ser Gln Ser Thr
```

```
                     110                  115                  120
        His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
                         125                  130                  135
 5
        Arg Ala Val Ala Ala Pro Thr Val Phe Ile Phe Pro Pro Ser Ser
                         140                  145                  150
        Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
 10                      155                  160                  165
        Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                         170                  175                  180
        Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 15         .                185                  190                  195
        Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
                         200                  205                  210
 20
        Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
                         215                  220                  225
        His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 25                      230                  235                  240
        Glu Cys
            242
 30     (2) INFORMATION FOR SEQ ID NO:43:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 762 base pairs
                (B) TYPE: Nucleic Acid
 35             (C) STRANDEDNESS: Double
                (D) TOPOLOGY: Linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
 40
        ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50
        TGCTACAAAC GCGTACGCTG AGATTCAGCT GCAGCAGTCT GGACCTGAGC 100
 45     TGATGAAGCC TGGGGCTTCA GTGAAGATAT CCTGCAAGGC TTCTGGTTAT 150
        TCATTCAGTA GCCACTACAT GCACTGGGTG AAGCAGAGCC ATGGAAAGAG 200
        CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA ACTACTTACA 250
 50     ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC 300
        ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA 350
 55     TTTCTGTGCA AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG 400
```

260

TCTGGGGCGC AGGGACCACG GTCACCGTCT CCTCCGCCTC CACCAAGGGC 450

CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC 500

AGCGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG 550

TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC CTTCCCGGCT 600

GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC 650

CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC 700

CCAGCAACAC CAAGGTGGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA 750

ACTCACACAT GA 762

(2) INFORMATION FOR SEQ ID NO:44:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 253 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
  1   5   10   .   15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Ile Gln Leu Gln Gln Ser
          20   25   30

Gly Pro Glu Leu Met Lys Pro Gly Ala Ser Val Lys Ile Ser Cys
          35   40   45

Lys Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val
          50   55   60

Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile Asp
          65   70   75

Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Lys
          80   85   90

Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Asn Val His
          95   100   105

Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys Ala
          110   115   120

Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp
          125   130   135

Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
          140   145   150

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly

261

```
                     155                160                165
     Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                     170                175                180
  5
     Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
                     185                190                195
     His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
 10                  200                205                210
     Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
                     215                220                225
 15  Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
                     230                235                240
     Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
                     245                250            253
 20
     (2) INFORMATION FOR SEQ ID NO:45:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 114 amino acids
 25          (B) TYPE: Amino Acid
             (D) TOPOLOGY: Linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

 30  Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu
       1               5                10                   15
     Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val
       .              20                25                   30
 35  His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
                     35                 40                   45
     Gly Gln Ser Pro Lys Leu Leu Ile Tyr Tyr Lys Val Ser Asn Arg
 40                  50                 55                   60
     Phe Ser Gly Val Pro Asp Arg Phe Ser Asp Ser Gly Ser Gly Thr
                     65                 70                   75
 45  Asp Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
                     80                 85                   90
     Leu Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly
                     95                 100                  105
 50
     Ala Gly Thr Lys Leu Glu Leu Lys Arg
                     110            114

     (2) INFORMATION FOR SEQ ID NO:46:
 55
         (i) SEQUENCE CHARACTERISTICS:
```

262

    (A) LENGTH: 114 amino acids
    (B) TYPE: Amino Acid
    (D) TOPOLOGY: Linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5               10                      15
```

10
```
Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val
                20               25                      30
```

```
His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro
                35               40                      45
```
15
```
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Lys Val Ser Asn Arg
                50               55                      60
```

```
Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
20              65               70                      75
```

```
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                80               85                      90
```

25
```
Thr Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly
                95               100                     105
```

```
Gln Gly Thr Lys Val Glu Ile Lys Arg
        .    110              114
```
30

(2) INFORMATION FOR SEQ ID NO:47:

    (i) SEQUENCE CHARACTERISTICS:
    . (A) LENGTH: 109 amino acids
35   (B) TYPE: PRT
    (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

40
```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5               10                      15
```

```
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Thr Ile Ser
                20               25                      30
```
45
```
Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
                35               40                      45
```

```
Leu Leu Ile Tyr Tyr Ser Gly Ser Thr Leu Glu Ser Gly Val Pro
50              50               55                      60
```

```
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
                65               70                      75
```

55
```
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
                80               85                      90
```

```
Gln His Asn Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val
                95                  100                 105

Glu Ile Lys Arg
                109
```

(2) INFORMATION FOR SEQ ID NO:48:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 117 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly
 1               5                  10                  15

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser
                20                  25                  30

Ser His Tyr Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu
                35                  40                  45

Glu Trp Ile Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr
                50                  55                  60

Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser
                65                  70                  75

Ser Ser Thr Ala Asn Val His Leu Ser Ser Leu Thr Ser Asp Asp
                80                  85                  90

Ser Ala Val Tyr Phe Cys Ala Ala Arg Gly Asp Tyr Arg Tyr Asn
                95                  100                 105

Gly Asp Trp Phe Phe Asp Val Trp Gly Ala Gly Thr
                110                 115     117
```

(2) INFORMATION FOR SEQ ID NO:49:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 117 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 1               5                  10                  15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe Ser
                20                  25                  30

Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
```

264

```
                        35                    40                    45
        Glu Trp Val Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr
                        50                    55                    60
5
        Asn Gln Lys Phe Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
                        65                    70                    75

        Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
10                      80                    85                    90

        Thr Ala Val Tyr Tyr Cys Ala Ala Arg Gly Asp Tyr Arg Tyr Asn
                        95                   100                   105

15      Gly Asp Trp Phe Phe Asp Val Trp Gly Gln Gly Thr
                       110                   115   117
```

(2) INFORMATION FOR SEQ ID NO:50:

20   (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 116 amino acids
            (B) TYPE: PRT
            (D) TOPOLOGY: Linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
        Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
        1               5                    10                    15

30      Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Thr
                        20                    25                    30

        Gly His Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
          .             35                    40                    45
35
        Glu Trp Val Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Tyr
                        50                    55                    60

        Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
40                      65                    70                    75

        Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
                        80                    85                    90

45      Thr Ala Val Tyr Tyr Cys Ala Ala Arg Gly Ile Tyr Phe Tyr Gly
                        95                   100                   105

        Thr Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
                       110                   115 116
50
```

(2) INFORMATION FOR SEQ ID NO:51:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 242 amino acids
55   (B) TYPE: Amino Acid
            (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1               5                   10                  15

Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser
                20                  25                  30

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
                35                  40                  45

Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Asn Thr Tyr
                50                  55                  60

Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
      ·         65                  70                  75

Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe
                80                  85                  90

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
                95                  100                 105

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Thr
                110                 115                 120

His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                125                 130                 135

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
                140                 145                 150

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
      ·         155                 160                 165

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                170                 175                 180

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                185                 190                 195

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
                200                 205                 210

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
                215                 220                 225

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                230                 235                 240

Glu Cys
242
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 253 amino acids
    (B) TYPE: Amino Acid
    (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1               5                  10                  15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser
                20                  25                  30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
                35                  40                  45

Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val
                50                  55                  60

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp
                65                  70                  75

Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg
                80                  85                  90

Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln
                95                  100                 105

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                110                 115                 120

Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp
                125                 130                 135

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
                140                 145                 150

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
                155                 160                 165

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                170                 175                 180

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
                185                 190                 195

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
                200                 205                 210

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
                215                 220                 225

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
                230                 235                 240

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
```

267

```
            245                 250          253
```

(2) INFORMATION FOR SEQ ID NO:53:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 159 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```
Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met
 1               5                   10                  15

Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn
                 20              25                  30

Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr
                 35              40                  45

Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly
                 50              55                  60

Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Ser
                 65              70                  75

Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu
                 80              85                  90

Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val
                 95              100                 105

Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe
                 110             115                 120

Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala
                 125             130                 135

Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe
                 140             145                 150

Ala Asn Ile Leu Arg Asn Lys Glu Ser
                 155             159
```

(2) INFORMATION FOR SEQ ID NO:54:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 780 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50
```

TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100

TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150

AGCTTAGTAC ATGGTATAGG TAACACGTAT TTACACTGGT ATCAACAGAA 200

ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250

CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300

CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350

ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400

TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450

GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500

CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550

CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600

TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650

CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700

CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750

CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

(2) INFORMATION FOR SEQ ID NO:55:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 253 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
1   5   10   15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
            20   25   30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
            35   40   45

Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val
            50   55   60

Lys Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp
            65   70   75

Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg

269

```
                    80                    85                    90

      Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln
                      95                   100                   105

      Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                     110                   115                   120

      Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp
                     125                   130                   135

      Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
                     140                   145                   150

      Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
                     155                   160                   165

      Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                     170                   175                   180

      Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
                     185                   190                   195

      His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
                     200                   205                   210

      Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
                     215                   220                   225

      Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
                     230                   235                   240

      Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
        .              245                   250             253
```

(2) INFORMATION FOR SEQ ID NO:56:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 242 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
      Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
        1               5                    10                   15

      Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser
                      20                    25                   30

      Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
                      35                    40                   45

      Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Ala Thr Tyr
                      50                    55                   60
```

```
Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
                65                  70                  75

Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe
                80                  85                  90

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
                95                  100                 105

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Thr
                110                 115                 120

His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                125                 130                 135

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
                140                 145                 150

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                155                 160                 165

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                170                 175                 180

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                185                 190                 195

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
                200                 205                 210

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
                215                 220                 225

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                230                 235                 240

Glu Cys
    242
```

(2) INFORMATION FOR SEQ ID NO:57:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Arg Met Lys
  1               5                   10                  15

Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His
                20                  25                  30

Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg
                35                  40                  45
```

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(2) INFORMATION FOR SEQ ID NO:58:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 780 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50

TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100

TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150

AGCTTAGTAC ATGGTATAGG TGCTACGTAT TTACACTGGT ATCAACAGAA 200

ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250

CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300

CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350

ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400

TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450

GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500

CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550

CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600

TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650

CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700

CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750

CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780
```

(2) INFORMATION FOR SEQ ID NO:59:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 927 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```
AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50
```

```
TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG 100

AGGTTCAGCT AGTGCAGTCT GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA 150

CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACTATAT 200

GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250

TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300

TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA 350

CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT 400

ATCGCTACAA TGGTGACTGG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450

GTCACCGTCT CCTCGGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500

ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550

TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600

CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT 650

CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700

AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTCGAC 750

AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCGCCGTG 800

CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA GAGGACAAGG 850

TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA 900

CTCAAAAAGC TTGTCGGGGA GCGCTAA 927
```

(2) INFORMATION FOR SEQ ID NO:60:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 298 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1           5                  10                  15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser
             20                  25                  30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
             35                  40                  45

Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val
```

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```
              50                    55                    60

      Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp
  5                   65                    70                    75

      Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg
                      80                    85                    90

      Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln
 10                   95                   100                   105

      Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                     110                   115                   120

 15   Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp
                     125                   130                   135

      Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
                     140                   145                   150

 20   Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
                     155                   160                   165

 25   Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                     170                   175                   180

      Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
                     185                   190                   195

 30   His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
                     200                   205                   210

      Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
                     215                   220                   225

 35   Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
                     230                   235                   240

      Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 40                  245                   250                   255

      Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Arg Met Lys Gln Leu
                     260                   265                   270

 45   Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu
                     275                   280                   285

      Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg
                     290                   295          298
 50
      (2) INFORMATION FOR SEQ ID NO:61:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 6563 base pairs
 55           (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
```

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

5

```
GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50

TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT 100

GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT 150

TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG 200

GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG 250

GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA 300

AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT 350

ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GAATTCGAGC 400

TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAAAGAAT 450

ATCGCATTTC TTCTTGCATC TATGTTCGTT TTTTCTATTG CTACAAACGC 500

ATACGCTGAT ATCCAGATGA CCCAGTCCCC GAGCTCCCTG TCCGCCTCTG 550

TGGGCGATAG GGTCACCATC ACCTGCAGGT CAAGTCAAAG CTTAGTACAT 600

GGTATAGGTG CTACGTATTT ACACTGGTAT CAACAGAAAC CAGGAAAAGC 650

TCCGAAACTA CTGATTTACA AAGTATCCAA TCGATTCTCT GGAGTCCCTT 700

CTCGCTTCTC TGGATCCGGT TCTGGGACGG ATTTCACTCT GACCATCAGC 750

AGTCTGCAGC CAGAAGACTT CGCAACTTAT TACTGTTCAC AGAGTACTCA 800

TGTCCCGCTC ACGTTTGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG 850

TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA 900

TCTGGAACTG CTTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA 950

GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC 1000

AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC 1050

AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC 1100

CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA 1150

ACAGGGGAGA GTGTTAAGCT GATCCTCTAC GCCGGACGCA TCGTGGCCCT 1200

AGTACGCAAC TAGTCGTAAA AAGGGTATCT AGAGGTTGAG GTGATTTTAT 1250

GAAAAAGAAT ATCGCATTTC TTCTTGCATC TATGTTCGTT TTTTCTATTG 1300
```

275

```
        CTACAAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTGG CGGTGGCCTG 1350

     5  GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT CTGGCTACTC 1400

        CTTCTCGAGT CACTATATGC ACTGGGTCCG TCAGGCCCCG GGTAAGGGCC 1450

        TGGAATGGGT TGGATATATT GATCCTTCCA ATGGTGAAAC TACGTATAAT 1500

    10  CAAAAGTTCA AGGGCCGTTT CACTTTATCT CGCGACAACT CCAAAAACAC 1550

        AGCATACCTG CAGATGAACA GCCTGCGTGC TGAGGACACT GCCGTCTATT 1600

        ACTGTGCAAG AGGGGATTAT CGCTACAATG GTGACTGGTT CTTCGACGTC 1650

    15  TGGGGTCAAG GAACCCTGGT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC 1700

        ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT GGGGGCACAG 1750

    20  CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 1800

        TCGTGGAACT CAGGCGCCCT GACCAGCGGC GTGCACACCT TCCCGGCTGT 1850

        CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACCGTGCCCT 1900

    25  CCAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA TCACAAGCCC 1950

        AGCAACACCA AGGTCGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAC 2000

    30  TCACACATGC CCGCCGTGCC CAGCACCAGA ACTGCTGGGC GGCCGCATGA 2050

        AACAGCTAGA GGACAAGGTC GAAGAGCTAC TCTCCAAGAA CTACCACCTA 2100

        GAGAATGAAG TGGCAAGACT CAAAAAGCTT GTCGGGGAGC GCTAAGCATG 2150

    35  CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCCGCCGGGC GTTTTTTATT 2200

        GTTAACTCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA TGCGGTAGTT 2250

    40  TATCACAGTT AAATTGCTAA CGCAGTCAGG CACCGTGTAT GAAATCTAAC 2300

        AATGCGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT 2350

        AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT ATCGTCCATT 2400

    45  CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG 2450

        ATGCAATTTC TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG 2500

    50  CCGCCGCCCA GTCCTGCTCG CTTCGCTACT TGGAGCCACT ATCGACTACG 2550

        CGATCATGGC GACCACACCC GTCCTGTGGA TCCTCTACGC CGGACGCATC 2600

        GTGGCCGGCA TCACCGGCGC CACAGGTGCG GTTGCTGGCG CCTATATCGC 2650

    55  CGACATCACC GATGGGGAAG ATCGGGCTCG CCACTTCGGG CTCATGAGCG 2700
```

276

```
CTTGTTTCGG CGTGGGTATG GTGGCAGGCC CCGTGGCCGG GGGACTGTTG 2750

GGCGCCATCT CCTTGCACGC ACCATTCCTT GCGGCGGCGG TGCTCAACGG 2800

CCTCAACCTA CTACTGGGCT GCTTCCTAAT GCAGGAGTCG CATAAGGGAG 2850

AGCGTCGTCC GATGCCCTTG AGAGCCTTCA ACCCAGTCAG CTCCTTCCGG 2900

TGGGCGCGGG GCATGACTAT CGTCGCCGCA CTTATGACTG TCTTCTTTAT 2950

CATGCAACTC GTAGGACAGG TGCCGGCAGC GCTCTGGGTC ATTTTCGGCG 3000

AGGACCGCTT TCGCTGGAGC GCGACGATGA TCGGCCTGTC GCTTGCGGTA 3050

TTCGGAATCT TGCACGCCCT CGCTCAAGCC TTCGTCACTG GTCCCGCCAC 3100

CAAACGTTTC GGCGAGAAGC AGGCCATTAT CGCCGGCATG GCGGCCGACG 3150

CGCTGGGCTA CGTCTTGCTG GCGTTCGCGA CGCGAGGCTG GATGGCCTTC 3200

CCCATTATGA TTCTTCTCGC TTCCGGCGGC ATCGGGATGC CCGCGTTGCA 3250

GGCCATGCTG TCCAGGCAGG TAGATGACGA CCATCAGGGA CAGCTTCAAG 3300

GATCGCTCGC GGCTCTTACC AGCCTAACTT CGATCACTGG ACCGCTGATC 3350

GTCACGGCGA TTTATGCCGC CTCGGCGAGC ACATGGAACG GGTTGGCATG 3400

GATTGTAGGC GCCGCCCTAT ACCTTGTCTG CCTCCCCGCG TTGCGTCGCG 3450

GTGCATGGAG CCGGGCCACC TCGACCTGAA TGGAAGCCGG CGGCACCTCG 3500

CTAACGGATT CACCACTCCA AGAATTGGAG CCAATCAATT CTTGCGGAGA 3550

ACTGTGAATG CGCAAACCAA CCCTTGGCAG AACATATCCA TCGCGTCCGC 3600

CATCTCCAGC AGCCGCACGC GGCGCATCTC GGGCAGCGTT GGGTCCTGGC 3650

CACGGGTGCG CATGATCGTG CTCCTGTCGT TGAGGACCCG GCTAGGCTGG 3700

CGGGGTTGCC TTACTGGTTA GCAGAATGAA TCACCGATAC GCGAGCGAAC 3750

GTGAAGCGAC TGCTGCTGCA AAACGTCTGC GACCTGAGCA ACAACATGAA 3800

TGGTCTTCGG TTTCCGTGTT TCGTAAAGTC TGGAAACGCG GAAGTCAGCG 3850

CCCTGCACCA TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC 3900

CTGTGGAACA CCTACATCTG TATTAACGAA GCGCTGGCAT TGACCCTGAG 3950

TGATTTTTCT CTGGTCCCGC CGCATCCATA CCGCCAGTTG TTTACCCTCA 4000

CAACGTTCCA GTAACCGGGC ATGTTCATCA TCAGTAACCC GTATCGTGAG 4050

CATCCTCTCT CGTTTCATCG GTATCATTAC CCCCATGAAC AGAAATTCCC 4100
```

277

CCTTACACGG AGGCATCAAG TGACCAAACA GGAAAAAACC GCCCTTAACA 4150

TGGCCCGCTT TATCAGAAGC CAGACATTAA CGCTTCTGGA GAAACTCAAC 4200

GAGCTGGACG CGGATGAACA GGCAGACATC TGTGAATCGC TTCACGACCA 4250

CGCTGATGAG CTTTACCGCA GCTGCCTCGC GCGTTTCGGT GATGACGGTG 4300

AAAACCTCTG ACACATGCAG CTCCCGGAGA CGGTCACAGC TTGTCTGTAA 4350

GCGGATGCCG GGAGCAGACA AGCCCGTCAG GGCGCGTCAG CGGGTGTTGG 4400

CGGGTGTCGG GGCGCAGCCA TGACCCAGTC ACGTAGCGAT AGCGGAGTGT 4450

ATACTGGCTT AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC 4500

ATATGCGGTG TGAAATACCG CACAGATGCG TAAGGAGAAA ATACCGCATC 4550

AGGCGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT CGGTCGTTCG 4600

GCTGCGGCGA GCGGTATCAG CTCACTCAAA GGCGGTAATA CGGTTATCCA 4650

CAGAATCAGG GGATAACGCA GGAAAGAACA TGTGAGCAAA AGGCCAGCAA 4700

AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT TCCATAGGCT 4750

CCGCCCCCCT GACGAGCATC ACAAAAATCG ACGCTCAAGT CAGAGGTGGC 4800

GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGAAGCTCC 4850

CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT ACCTGTCCGC 4900

CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA CGCTGTAGGT 4950

ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA 5000

CCCCCCGTTC AGCCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA 5050

GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA GCCACTGGTA 5100

ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG 5150

TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC 5200

TCTGCTGAAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG 5250

GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTTGTTTG CAAGCAGCAG 5300

ATTACGCGCA GAAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC 5350

GGGGTCTGAC GCTCAGTGGA ACGAAAACTC ACGTTAAGGG ATTTTGGTCA 5400

TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA 5450

AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA 5500

CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT 5550

CATCCATAGT TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG 5600

GGCTTACCAT CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCACGCTC 5650

ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC 5700

GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT 5750

TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT 5800

TGTTGCCATT GCTGCAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG 5850

CTTCATTCAG CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC 5900

ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC GGTCCTCCGA TCGTTGTCAG 5950

AAGTAAGTTG GCCGCAGTGT TATCACTCAT GGTTATGGCA GCACTGCATA 6000

ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG 6050

TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC 6100

TTGCCCGGCG TCAACACGGG ATAATACCGC GCCACATAGC AGAACTTTAA 6150

AAGTGCTCAT CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC 6200

TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAACTG 6250

ATCTTCAGCA TCTTTTACTT TCACCAGCGT·TTCTGGGTGA GCAAAAACAG 6300

GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA 6350

ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA 6400

TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA 6450

TAGGGGTTCC GCGCACATTT CCCCGAAAAG TGCCACCTGA CGTCTAAGAA 6500

ACCATTATTA TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC 6550

CTTTCGTCTT CAA 6563

(2) INFORMATION FOR SEQ ID NO:62:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 242 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
  1   5   10   15

279

```
      Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser
                      20                  25                  30

 5    Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
                      35                  40                  45

      Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Glu Thr Tyr
                      50                  55                  60
10
      Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
                      65                  70                  75

      Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe
15                    80                  85                  90

      Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
                      95                  100                 105

20    Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Thr
                      110                 115                 120

      His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                      125                 130                 135
25
      Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
                      140                 145                 150

      Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
30    .                 155                 160                 165

      Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                      170                 175                 180

35    Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                      185                 190                 195

      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
                      200                 205                 210
40
      Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
                      215                 220                 225

      His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
45                    230                 235                 240

      Glu Cys
          242
```

50   (2) INFORMATION FOR SEQ ID NO:63:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 27 base pairs
          (B) TYPE: Nucleic Acid
55   (C) STRANDEDNESS: Single
          (D) TOPOLOGY: Linear

280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

5   CATGGTATAG GTTAAACTTA TTTACAC 27

(2) INFORMATION FOR SEQ ID NO:64:

    (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 27 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

    CATGGTATAG GTNNSACTTA TTTACAC 27

20 (2) INFORMATION FOR SEQ ID NO:65:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 780 base pairs
       (B) TYPE: Nucleic Acid
25   (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

30
ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50

TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100

TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150

AGCTTAGTAC ATGGTATAGG TGAGACGTAT TTACACTGGT ATCAACAGAA 200

ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250

CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300

CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350

ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400

TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450

GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500

CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550

CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600

TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650

281

CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700

CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750

5   CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

    (2) INFORMATION FOR SEQ ID NO:66:

        (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 78 base pairs
                (B) TYPE: Nucleic Acid
                (C) STRANDEDNESS: Single
                (D) TOPOLOGY: Linear

15   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

    CTAGTGCAGT CTGGCGGTGG CCTGGTGCAG CCAGGGGGCT CACTCCGTTT 50

20 GTCCTGTGCA GCTTCTGGCT ACTCCTTC 78

    (2) INFORMATION FOR SEQ ID NO:67:

        (i) SEQUENCE CHARACTERISTICS:
25   (A) LENGTH: 82 base pairs
                (B) TYPE: Nucleic Acid
                (C) STRANDEDNESS: Single
                (D) TOPOLOGY: Linear

30   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

    TCGAGAAGGA GTAGCCAGAA GCTGCACAGG ACAAACGGAG TGAGCCCCCT 50

35 GGCTGCACCA GGCCACCGCC AGACTGCACT AG 82

    (2) INFORMATION FOR SEQ ID NO:68:

        (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 8120 base pairs
                (B) TYPE: Nucleic Acid
                (C) STRANDEDNESS: Single
                (D) TOPOLOGY: Linear

45   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

    TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGATC GACAGCTGTG 50

50 GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCAGGCTCC CCAGCAGGCA 100

    GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG 150

    TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA 200
55
    GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC 250

282

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        CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT 300

   5    TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG 350

        AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTA GCTTATCCGG 400

        CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTGACGTAA 450

  10    GTACCGCCTA TAGAGCGATA AGAGGATTTT ATCCCCGCTG CCATCATGGT 500

        TCGACCATTG AACTGCATCG TCGCCGTGTC CCAAAATATG GGGATTGGCA 550

        AGAACGGAGA CCTACCCTGG CCTCCGCTCA GGAACGAGTT CAAGTACTTC 600

  15    CAAAGAATGA CCACAACCTC TTCAGTGGAA GGTAAACAGA ATCTGGTGAT 650

        TATGGGTAGG AAAACCTGGT CTCCATTCC TGAGAAGAAT CGACCTTTAA 700

  20    AGGACAGAAT TAATATAGTT CTCAGTAGAG AACTCAAAGA ACCACCACGA 750

        GGAGCTCATT TTCTTGCCAA AAGTTTGGAT GATGCCTTAA GACTTATTGA 800

        ACAACCGGAA TTGGCAAGTA AAGTAGACAT GGTTTGGATA GTCGGAGGCA 850

  25    GTTCTGTTTA CCAGGAAGCC ATGAATCAAC CAGGCCACCT TAGACTCTTT 900

        GTGACAAGGA TCATGCAGGA ATTTGAAAGT GACACGTTTT TCCCAGAAAT 950

  30    TGATTTGGGG AAATATAAAC CTCTCCCAGA ATACCCAGGC GTCCTCTCTG 1000

        AGGTCCAGGA GGAAAAAGGC ATCAAGTATA AGTTTGAAGT CTACGAGAAG 1050

        AAAGACTAAC AGGAAGATGC TTTCAAGTTC TCTGCTCCCC TCCTAAAGCT 1100

  35    ATGCATTTTT ATAAGACCAT GGGACTTTTG CTGGCTTTAG ATCCCCTTGG 1150

        CTTCGTTAGA ACGCAGCTAC AATTAATACA TAACCTTATG TATCATACAC 1200

  40    ATACGATTTA GGTGACACTA TAGATAACAT CCACTTTGCC TTTCTCTCCA 1250

        CAGGTGTCCA CTCCCAGGTC CAACTGCACC TCGGTTCTAT CGATTGAATT 1300

        CCACCATGGG ATGGTCATGT ATCATCCTTT TTCTAGTAGC AACTGCAACT 1350

  45    GGAGTACATT CAGAAGTTCA GCTAGTGCAG TCTGGCGGTG GCCTGGTGCA 1400

        GCCAGGGGGC TCACTCCGTT TGTCCTGTGC AGCTTCTGGC TACTCCTTCT 1450

  50    CGAGTCACTA TATGCACTGG GTCCGTCAGG CCCCGGGTAA GGGCCTGGAA 1500

        TGGGTTGGAT ATATTGATCC TTCCAATGGT GAAACTACGT ATAATCAAAA 1550

        GTTCAAGGGC CGTTTCACTT TATCTCGCGA CAACTCCAAA AACACAGCAT 1600

  55    ACCTGCAGAT GAACAGCCTG CGTGCTGAGG ACACTGCCGT CTATTACTGT 1650
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GCAAGAGGGG ATTATCGCTA CAATGGTGAC TGGTTCTTCG ACGTCTGGGG 1700

TCAAGGAACC CTGGTCACCG TCTCCTCGGC CTCCACCAAG GGCCCATCGG 1750

TCTTCCCCCT GGCACCCTCC TCCAAGAGCA CCTCTGGGGG CACAGCGGCC 1800

CTGGGCTGCC TGGTCAAGGA CTACTTCCCC GAACCGGTGA CGGTGTCGTG 1850

GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG GCTGTCCTAC 1900

AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGACTGT GCCCTCTAGC 1950

AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA 2000

CACCAAGGTG GACAAGAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACA 2050

CATGCCCACC GTGCCCAGCA CCTGAACTCC TGGGGGGACC GTCAGTCTTC 2100

CTCTTCCCCC CAAAACCCAA GGACACCCTC ATGATCTCCC GGACCCCTGA 2150

GGTCACATGC GTGGTGGTGG ACGTGAGCCA CGAAGACCCT GAGGTCAAGT 2200

TCAACTGGTA CGTGGACGGC GTGGAGGTGC ATAATGCCAA GACAAAGCCG 2250

CGGGAGGAGC AGTACAACAG CACGTACCGT GTGGTCAGCG TCCTCACCGT 2300

CCTGCACCAG GACTGGCTGA ATGGCAAGGA GTACAAGTGC AAGGTCTCCA 2350

ACAAAGCCCT CCCAGCCCCC ATCGAGAAAA CCATCTCCAA AGCCAAAGGG 2400

CAGCCCCGAG AACCACAGGT GTACACCCTG CCCCCATCCC GGGAAGAGAT 2450

GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC TTCTATCCCA 2500

GCGACATCGC CGTGGAGTGG GAGAGCAATG GCAGCCGGA GAACAACTAC 2550

AAGACCACGC CTCCCGTGCT GGACTCCGAC GGCTCCTTCT TCCTCTACAG 2600

CAAGCTCACC GTGGACAAGA GCAGGTGGCA GCAGGGGAAC GTCTTCTCAT 2650

GCTCCGTGAT GCATGAGGCT CTGCACAACC ACTACACGCA GAAGAGCCTC 2700

TCCCTGTCTC CGGGTAAATG AGTGCGACGG CCCTAGAGTC GACCTGCAGA 2750

AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA 2800

AATAAAGCAA TAGCATCACA AATTTCACAA ATAAAGCATT TTTTTCACTG 2850

CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG 2900

GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA AATAACCTCT 2950

GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA ACCATCTGTG 3000

GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA 3050
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      GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG 3100

      TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA 3150

      GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC 3200

      CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT 3250

      TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG 3300

      AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTA GCTTATCCGG 3350

      CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTCAGGTAA 3400

      GTACCGCCTA TAGAGTCTAT AGGCCCACCC CCTTGGCTTC GTTAGAACGC 3450

      GGCTACAATT AATACATAAC CTTTTGGATC GATCCTACTG ACACTGACAT 3500

      CCACTTTTTC TTTTTCTCCA CAGGTGTCCA CTCCCAGGTC CAACTGCACC 3550

      TCGGTTCGCG AAGCTAGCTT GGGCTGCATC GATTGAATTC CACCATGGGA 3600

      TGGTCATGTA TCATCCTTTT TCTAGTAGCA ACTGCAACTG GAGTACATTC 3650

      AGATATCCAG ATGACCCAGT CCCCGAGCTC CCTGTCCGCC TCTGTGGGCG 3700

      ATAGGGTCAC CATCACCTGC AGGTCAAGTC AAAGCTTAGT ACATGGTATA 3750

      GGTGCTACGT ATTTACACTG GTATCAACAG AAACCAGGAA AAGCTCCGAA 3800

      ACTACTGATT TACAAAGTAT CCAATCGATT CTCTGGAGTC CCTTCTCGCT 3850

      TCTCTGGATC CGGTTCTGGG ACGGATTTCA CTCTGACCAT CAGCAGTCTG 3900

      CAGCCAGAAG ACTTCGCAAC TTATTACTGT TCACAGAGTA CTCATGTCCC 3950

      GCTCACGTTT GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG 4000

      CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA 4050

      ACTGCTTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA 4100

      AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA 4150

      GTGTCACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC 4200

      CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA 4250

      AGTCACCCAT CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG 4300

      GAGAGTGTTA AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT 4350

      AATGGTTACA AATAAAGCAA TAGCATCACA AATTTCACAA ATAAAGCATT 4400

      TTTTTCACTG CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT 4450
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      ATCATGTCTG GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA 4500

      AATAACCTCT GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA 4550

      ACCAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC 4600

      CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG 4650

      GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC 4700

      ATCTCAATTA GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG 4750

      CCCCTAACTC CGCCCAGTTC CGCCCATTCT CCGCCCCATG CTGACTAAT 4800

      TTTTTTATT TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC 4850

      AGAAGTAGTG AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTG 4900

      TTACCTCGAG CGGCCGCTTA ATTAAGGCGC GCCATTTAAA TCCTGCAGGT 4950

      AACAGCTTGG CACTGGCCGT CGTTTTACAA CGTCGTGACT GGGAAAACCC 5000

      TGGCGTTACC CAACTTAATC GCCTTGCAGC ACATCCCCCC TTCGCCAGCT 5050

      GGCGTAATAG CGAAGAGGCC CGCACCGATC GCCCTTCCCA ACAGTTGCGT 5100

      AGCCTGAATG GCGAATGGCG CCTGATGCGG TATTTTCTCC TTACGCATCT 5150

      GTGCGGTATT TCACACCGCA TACGTCAAAG CAACCATAGT ACGCGCCCTG 5200

      TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT GGTTACGCGC AGCGTGACCG 5250

      CTACACTTGC CAGCGCCCTA GCGCCCGCTC CTTTCGCTTT CTTCCCTTCC 5300

      TTTCTCGCCA CGTTCGCCGG CTTTCCCCGT CAAGCTCTAA ATCGGGGGCT 5350

      CCCTTTAGGG TTCCGATTTA GTGCTTTACG GCACCTCGAC CCCAAAAAAC 5400

      TTGATTTGGG TGATGGTTCA CGTAGTGGGC CATCGCCCTG ATAGACGGTT 5450

      TTTCGCCCTT TGACGTTGGA GTCCACGTTC TTTAATAGTG GACTCTTGTT 5500

      CCAAACTGGA ACAACACTCA ACCCTATCTC GGGCTATTCT TTTGATTTAT 5550

      AAGGGATTTT GCCGATTTCG GCCTATTGGT TAAAAAATGA GCTGATTTAA 5600

      CAAAAATTTA ACGCGAATTT TAACAAAATA TTAACGTTTA CAATTTTATG 5650

      GTGCACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAACTCC 5700

      GCTATCGCTA CGTGACTGGG TCATGGCTGC GCCCCGACAC CCGCCAACAC 5750

      CCGCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGGCATC CGCTTACAGA 5800

      CAAGCTGTGA CCGTCTCCGG GAGCTGCATG TGTCAGAGGT TTTCACCGTC 5850
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ATCACCGAAA CGCGCGAGGC AGTATTCTTG AAGACGAAAG GGCCTCGTGA 5900

TACGCCTATT TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG 5950

TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT 6000

TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGAT 6050

AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTC 6100

CGTGTCGCCC TTATTCCCTT TTTTGCGGCA TTTTGCCTTC CTGTTTTTGC 6150

TCACCCAGAA ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG 6200

CACGAGTGGG TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG 6250

AGTTTTCGCC CCGAAGAACG TTTTCCAATG ATGAGCACTT TTAAAGTTCT 6300

GCTATGTGGC GCGGTATTAT CCCGTGATGA CGCCGGGCAA GAGCAACTCG 6350

GTCGCCGCAT ACACTATTCT CAGAATGACT TGGTTGAGTA CTCACCAGTC 6400

ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC 6450

TGCCATAACC ATGAGTGATA ACACTGCGGC CAACTTACTT CTGACAACGA 6500

TCGGAGGACC GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT 6550

GTAACTCGCC TTGATCGTTG GGAACCGGAG CTGAATGAAG CCATACCAAA 6600

CGACGAGCGT GACACCACGA TGCCAGCAGC AATGGCAACA ACGTTGCGCA 6650

AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA ACAATTAATA 6700

GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACTTCTGC GCTCGGCCCT 6750

TCCGGCTGGC TGGTTTATTG CTGATAAATC TGGAGCCGGT GAGCGTGGGT 6800

CTCGCGGTAT CATTGCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC 6850

GTAGTTATCT ACACGACGGG GAGTCAGGCA ACTATGGATG AACGAAATAG 6900

ACAGATCGCT GAGATAGGTG CCTCACTGAT TAAGCATTGG TAACTGTCAG 6950

ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT TCATTTTTAA 7000

TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT 7050

CCCTTAACGT GAGTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA 7100

TCAAAGGATC TTCTTGAGAT CCTTTTTTTC TGCGCGTAAT CTGCTGCTTG 7150

CAAACAAAAA AACCACCGCT ACCAGCGGTG GTTTGTTTGC CGGATCAAGA 7200

GCTACCAACT CTTTTTCCGA AGGTAACTGG CTTCAGCAGA GCGCAGATAC 7250

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CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAAGAAC 7300

TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC 7350

TGCTGCCAGT GGCGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT 7400

AGTTACCGGA TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA 7450

CAGCCCAGCT TGGAGCGAAC GACCTACACC GAACTGAGAT ACCTACAGCG 7500

TGAGCATTGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT 7550

ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA 7600

GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG 7650

ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA 7700

AAAACGCCAG CAACGCGGCC TTTTTACGGT TCCTGGCCTT TTGCTGGCCT 7750

TTTGCTCACA TGTTCTTTCC TGCGTTATCC CCTGATTCTG TGGATAACCG 7800

TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCCGCAGC CGAACGACCG 7850

AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC AATACGCAAA 7900

CCGCCTCTCC CCGCGCGTTG GCCGATTCAT TAATCCAGCT GGCACGACAG 7950

GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT 8000

ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT 8050

ATGTTGTGTG GAATTGTGAG CGGATAACAA TTTCACACAG GAAACAGCTA 8100

TGACCATGAT TACGAATTAA 8120
```

(2) INFORMATION FOR SEQ ID NO:69:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 800 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50

TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG 100

AGGTTCAGCT AGTGCAGTCT GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA 150

CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACTATAT 200
```

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GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250

TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300

TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA 350

CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT 400

ATCGCTACAA TGGTGACTGG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450

GTCACCGTCT CCTCGGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500

ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550

TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600

CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT 650

CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700

AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTCGAC 750

AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCGCCTGA 800

(2) INFORMATION FOR SEQ ID NO:70:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 256 amino acids
       (B) TYPE: Amino Acid
       (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1               5                  10                  15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser
                 20                  25                  30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
                 35                  40                  45

Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val
                 50                  55                  60

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp
                 65                  70                  75

Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg
                 80                  85                  90

Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln
                 95                 100                 105

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                110                 115                 120
```

```
      Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp
                      125                 130                 135

  5   Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
                      140                 145                 150

      Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
                      155                 160                 165
 10
      Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                      170                 175                 180

      Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 15                   185                 190                 195

      His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
                      200                 205                 210

 20   Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
                      215                 220                 225

      Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
                      230                 235                 240
 25
      Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
                      245                 250                 255

      Pro
 30   256

      (2) INFORMATION FOR SEQ ID NO:71:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 452 amino acids
 35           (B) TYPE: Amino Acid
              (D) TOPOLOGY: Linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
 40
      Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly
        1               5                  10                  15

 45   Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe Ser
                       20                  25                  30

      Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
                       35                  40                  45

 50   Glu Trp Val Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr
                       50                  55                  60

      Asn Gln Lys Phe Lys Gly Arg Phe Thr Leu Ser Arg Asp Asn Ser
                       65                  70                  75
 55
      Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
```

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	80				85				90

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Asp Tyr Arg Tyr Asn Gly
                    95   100   105

Asp Trp Phe Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
                    110   115   120

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
                    125   130   135

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
                    140   145   150

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
                    155   160   165

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                    170   175   180

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
                    185   190   195

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
                    200   205   210

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
                    215   220   225

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                    230   235   240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                    245   250   255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
                    260   265   270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
                    275   280   285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
                    290   295   300

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                    305   310   315

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                    320   325   330

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
                    335   340   345

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
                    350   355   360

```
Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                365             370             375

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                380             385             390

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                395             400             405

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                410             415             420

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
                425             430             435

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
                440             445             450

Gly Lys
    452
```

(2) INFORMATION FOR SEQ ID NO:72:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 219 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1               5               10              15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val
                20              25              30

His Gly Ile Gly Ala Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro
                35              40              45

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
                50              55              60

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                65              70              75

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
                80              85              90

Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly Gln
                95              100             105

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
                110             115             120

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
                125             130             135
```

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```
    Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
                    140                 145                 150

5   Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
                    155                 160                 165

    Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                    170                 175                 180
10
    Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
                    185                 190                 195

    Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
15                  200                 205                 210

    Thr Lys Ser Phe Asn Arg Gly Glu Cys
                    215             219
```